

## Supporting information

SWISS-MODEL is an automated structure-homology modeling server that is available through the ExPASy web server.<sup>84</sup> The sequence for each bacteriocin was uploaded to the server followed by an automated search through the Research Collaboratory Structural Bioinformatics' (RCSB) Protein Data Bank (PDB) for a homologous peptide with an experimentally determined structure.<sup>85</sup> PDB coordinates of the peptide with the highest sequence-homology were used to create a structural model of each bacteriocin of interest.

### 1. Pneumocyclin

#### A) PDB file for model of pneumocyclin. Structure modeled after NKR-5-3B using SWISS-MODEL<sup>84</sup>

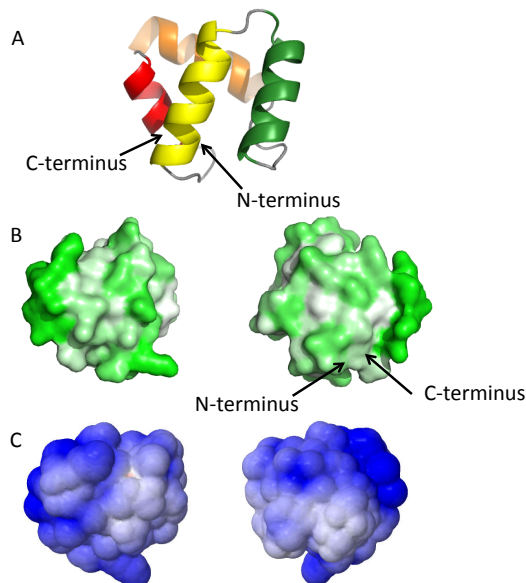
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CASSARINO,M.BERTONI,L.BORDOLI,
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AND QUATERNARY
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JRNL REF NUCLEIC.ACIDS.RES 2014
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JRNL PMID 24782522
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```







B)



**Figure S1-** Structural models of pneumocyclin. A) Ribbon diagram depicting the saposin-like fold. The C- and N- termini are explicitly shown. Hydrophobic surface (B) and electrostatic potential surface (C) maps of pneumocyclin. Orientation peptide backbone in surface filling diagrams, B and C, correlate to one another.

## 2. Aureocyclin

### A) PDB file for model of aureocyclin. Structure modeled after NKR-5-3B using SWISS-MODEL.<sup>84</sup>

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M.BIASINI,S.BIENERT,A.WATERHOUSE,K.ARNOLD,G.STUDER,
JRNL    AUTH 2 T.SCHMIDT,F.KIEFER,T.GALLO
CASSARINO,M.BERTONI,L.BORDOLI,
JRNL    AUTH 3 T.SCHWEDE
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AND QUATERNARY
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INFORMATION
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JRNL    PMID 24782522
JRNL    DOI 10.1093/nar/gku340
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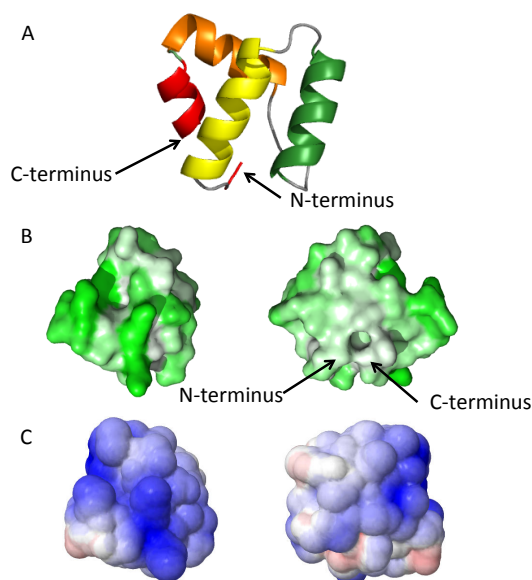








B)



**Figure S2-** Structural models of aureocyclin. A) Ribbon diagram depicting the saaposin-like fold. The C- and N- termini are explicitly shown. Hydrophobic surface (B) and electrostatic potential surface (C) maps of aureocyclin. Orientation peptide backbone in the space filling diagrams, B and C, correlate to one another.

### 3) Amylocyclin

#### A) PDB file for model of amylocyclin. Structure modeled after NKR-5-3B using SWISS-MODEL<sup>84</sup>

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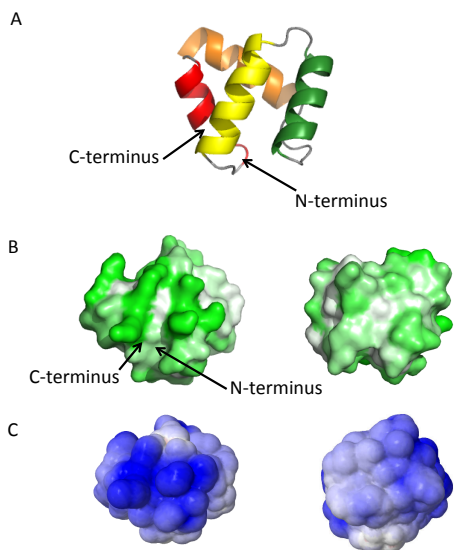






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ATOM	402	C	LYS	A	59	9.297	1.852	-3.979	1.00	0.74	C	ATOM	428	C	ALA	A	62	6.975	-2.370	-2.670	1.00	0.81	C
ATOM	403	O	LYS	A	59	9.439	0.631	-3.933	1.00	0.74	O	ATOM	429	O	ALA	A	62	6.441	-3.444	-2.388	1.00	0.81	O
ATOM	404	CB	LYS	A	59	9.763	2.913	-6.218	1.00	0.74	C	ATOM	430	CB	ALA	A	62	6.379	-0.867	-4.633	1.00	0.81	C
ATOM	405	CG	LYS	A	59	10.534	1.711	-6.775	1.00	0.74	C	ATOM	431	N	ALA	A	63	8.294	-2.146	-2.479	1.00	0.74	N
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ATOM	409	N	TYR	A	60	9.672	2.640	-2.943	1.00	0.73	N	ATOM	435	CB	ALA	A	63	10.698	-2.625	-2.198	1.00	0.74	C
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ATOM	414	CG	TYR	A	60	10.969	2.759	0.636	1.00	0.73	C	ATOM	440	CB	TRP	A	64	8.153	-1.391	2.462	1.00	0.68	C
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ATOM	416	CD2	TYR	A	60	12.291	2.418	0.922	1.00	0.73	C	ATOM	442	CD1	TRP	A	64	8.478	-1.452	5.032	1.00	0.68	C
ATOM	417	CE1	TYR	A	60	10.326	1.985	2.857	1.00	0.73	C	ATOM	443	CD2	TRP	A	64	6.315	-1.328	4.454	1.00	0.68	C
ATOM	418	CE2	TYR	A	60	12.634	1.883	2.171	1.00	0.73	C	ATOM	444	NE1	TRP	A	64	7.729	-1.553	6.184	1.00	0.68	N
ATOM	419	CZ	TYR	A	60	11.650	1.665	3.139	1.00	0.73	C	ATOM	445	CE2	TRP	A	64	6.402	-1.510	5.845	1.00	0.68	C
ATOM	420	OH	TYR	A	60	11.978	1.136	4.399	1.00	0.73	O	ATOM	446	CE3	TRP	A	64	5.065	-1.252	3.833	1.00	0.68	C
ATOM	421	N	ALA	A	61	7.845	1.928	-0.919	1.00	0.83	N	ATOM	447	CZ2	TRP	A	64	5.263	-1.632	6.634	1.00	0.68	C
ATOM	422	CA	ALA	A	61	6.727	1.299	-0.271	1.00	0.83	C	ATOM	448	CZ3	TRP	A	64	3.917	-1.357	4.635	1.00	0.68	C
ATOM	423	C	ALA	A	61	6.279	0.047	-1.009	1.00	0.83	C	ATOM	449	CH2	TRP	A	64	4.013	-1.554	6.012	1.00	0.68	C
ATOM	424	O	ALA	A	61	5.865	-0.907	-0.399	1.00	0.83	O	ATOM	450	OXT	TRP	A	64	7.105	-3.771	3.364	1.00	0.68	O
ATOM	425	CB	ALA	A	61	5.554	2.258	-0.038	1.00	0.83	C	TER	451	TRP	A	64							
ATOM	426	N	ALA	A	62	6.420	0.008	-2.359	1.00	0.81	N	END											

B)



**Figure S3-** Structural models of amylocyclin. A) Ribbon diagram depicting the saposin-like fold. The C- and N- termini are explicitly shown. Hydrophobic surface (B) and electrostatic potential surface (C) maps of amylocyclin. Orientation peptide backbone in surface filling diagrams, B and C, correlate to one another.

## 4. Leucocyclin

### A) PDB file for model of leucocyclin. Structure modeled after NKR-5-3B using SWISS-MODEL<sup>84</sup>

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TITLE 2 Untitled Project

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ATOM 34 CA GLY A 8 4.078 -11.358 1.238 1.00 0.84 C  
ATOM 35 C GLY A 8 3.291 -11.435 -0.053 1.00 0.84 C  
ATOM 36 O GLY A 8 2.777 -12.482 -0.433 1.00 0.84 O  
ATOM 37 N ILE A 9 3.178 -10.295 -0.762 1.00 0.74 N  
ATOM 38 CA ILE A 9 2.358 -10.123 -1.953 1.00 0.74 C  
ATOM 39 C ILE A 9 3.261 -9.955 -3.155 1.00 0.74 C  
ATOM 40 O ILE A 9 4.470 -9.792 -3.030 1.00 0.74 O  
ATOM 41 CB ILE A 9 1.389 -8.937 -1.886 1.00 0.74 C  
ATOM 42 CG1 ILE A 9 2.096 -7.573 -1.668 1.00 0.74 C  
ATOM 43 CG2 ILE A 9 0.341 -9.282 -0.809 1.00 0.74 C  
ATOM 44 CD1 ILE A 9 1.145 -6.372 -1.740 1.00 0.74 C  
ATOM 45 N SER A 10 2.716 -9.983 -4.385 1.00 0.84 N  
ATOM 46 CA SER A 10 3.498 -9.716 -5.582 1.00 0.84 C  
ATOM 47 C SER A 10 3.818 -8.237 -5.768 1.00 0.84 C  
ATOM 48 O SER A 10 3.170 -7.356 -5.205 1.00 0.84 O  
ATOM 49 CB SER A 10 2.815 -10.254 -6.872 1.00 0.84 C  
ATOM 50 OG SER A 10 1.608 -9.550 -7.183 1.00 0.84 O  
ATOM 51 N LYS A 11 4.836 -7.912 -6.598 1.00 0.75 N  
ATOM 52 CA LYS A 11 5.141 -6.542 -6.998 1.00 0.75 C  
ATOM 53 C LYS A 11 4.009 -5.882 -7.773 1.00 0.75 C  
ATOM 54 O LYS A 11 3.780 -4.682 -7.657 1.00 0.75 O  
ATOM 55 CB LYS A 11 6.451 -6.462 -7.812 1.00 0.75 C  
ATOM 56 CG LYS A 11 7.688 -6.849 -6.989 1.00 0.75 C  
ATOM 57 CD LYS A 11 8.973 -6.781 -7.829 1.00 0.75 C  
ATOM 58 CE LYS A 11 10.235 -7.150 -7.042 1.00 0.75 C  
ATOM 59 NZ LYS A 11 11.427 -7.101 -7.920 1.00 0.75 N  
ATOM 60 N SER A 12 3.258 -6.688 -8.555 1.00 0.80 N  
ATOM 61 CA SER A 12 2.033 -6.277 -9.237 1.00 0.80 C  
ATOM 62 C SER A 12 0.972 -5.789 -8.262 1.00 0.80 C  
ATOM 63 O SER A 12 0.479 -4.668 -8.358 1.00 0.80 O  
ATOM 64 CB SER A 12 1.435 -7.471 -10.037 1.00 0.80 C  
ATOM 65 OG SER A 12 0.272 -7.104 -10.780 1.00 0.80 O  
ATOM 66 N LEU A 13 0.665 -6.598 -7.223 1.00 0.74 N  
ATOM 67 CA LEU A 13 -0.262 -6.215 -6.176 1.00 0.74 C  
ATOM 68 C LEU A 13 0.219 -5.013 -5.384 1.00 0.74 C  
ATOM 69 O LEU A 13 -0.549 -4.105 -5.102 1.00 0.74 O  
ATOM 70 CB LEU A 13 -0.545 -7.394 -5.216 1.00 0.74 C  
ATOM 71 CG LEU A 13 -1.354 -8.558 -5.825 1.00 0.74 C  
ATOM 72 CD1 LEU A 13 -1.357 -9.751 -4.856 1.00 0.74 C  
ATOM 73 CD2 LEU A 13 -2.793 -8.151 -6.180 1.00 0.74 C  
ATOM 74 N ALA A 14 1.510 -4.950 -5.033 1.00 0.80 N  
ATOM 75 CA ALA A 14 2.100 -3.826 -4.340 1.00 0.80 C  
ATOM 76 C ALA A 14 2.080 -2.489 -5.070 1.00 0.80 C  
ATOM 77 O ALA A 14 1.812 -1.452 -4.472 1.00 0.80 O  
ATOM 78 CB ALA A 14 3.539 -4.194 -4.023 1.00 0.80 C  
ATOM 79 N ASN A 15 2.340 -2.481 -6.388 1.00 0.75 N  
ATOM 80 CA ASN A 15 2.139 -1.334 -7.252 1.00 0.75 C  
ATOM 81 C ASN A 15 0.660 -0.912 -7.330 1.00 0.75 C  
ATOM 82 O ASN A 15 0.310 0.266 -7.333 1.00 0.75 O  
ATOM 83 CB ASN A 15 2.721 -1.677 -8.640 1.00 0.75 C  
ATOM 84 CG ASN A 15 2.786 -0.425 -9.501 1.00 0.75 C  
ATOM 85 OD1 ASN A 15 3.420 0.567 -9.143 1.00 0.75 O  
ATOM 86 ND2 ASN A 15 2.100 -0.448 -10.664 1.00 0.75 N  
ATOM 87 N THR A 16 -0.264 -1.885 -7.368 1.00 0.75 N  
ATOM 88 CA THR A 16 -1.702 -1.639 -7.239 1.00 0.75 C  
ATOM 89 C THR A 16 -2.102 -1.044 -5.891 1.00 0.75 C  
ATOM 90 O THR A 16 -2.887 -0.096 -5.825 1.00 0.75 O  
ATOM 91 CB THR A 16 -2.510 -2.892 -7.528 1.00 0.75 C  
ATOM 92 OG1 THR A 16 -2.318 -3.274 -8.883 1.00 0.75 O  
ATOM 93 CG2 THR A 16 -4.016 -2.666 -7.365 1.00 0.75 C  
ATOM 94 N ILE A 17 -1.528 -1.543 -4.769 1.00 0.69 N  
ATOM 95 CA ILE A 17 -1.676 -0.970 -3.424 1.00 0.69 C  
ATOM 96 C ILE A 17 -1.184 0.439 -3.400 1.00 0.69 C  
ATOM 97 O ILE A 17 -1.841 1.343 -2.892 1.00 0.69 O  
ATOM 98 CB ILE A 17 -0.878 -1.709 -2.344 1.00 0.69 C  
ATOM 99 CG1 ILE A 17 -1.422 -3.121 -2.103 1.00 0.69 C

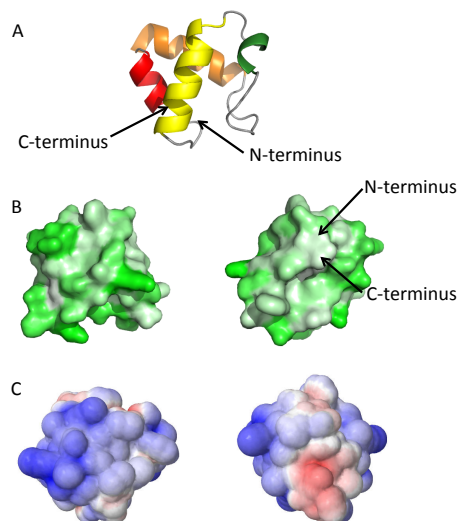








B)



**Figure S4-** Structural models of leucocyclicin. A) Ribbon diagram depicting the saposin-like fold. The C- and N- termini are explicitly shown. Hydrophobic surface (B) and electrostatic potential surface (C) maps of leucocyclicin. Orientation peptide backbone in surface filling diagrams, B and C, correlate to one another.

## 5. Garvacin ML

### A) PDB file for model of garvacin ML. Structure modeled after AS-48 using SWISS-MODEL<sup>84</sup>

```

TITLE  SWISS-MODEL SERVER (https://swissmodel.expasy.org)
TITLE  2 Untitled Project
EXPDTA  THEORETICAL MODEL (SWISS-MODEL SERVER)
AUTHOR  SWISS-MODEL SERVER (SEE REFERENCE IN JRNL
Records)
REVDAT  1 11-AUG-16 1MOD  1  22:28
JRNL  AUTH
M.BIASINI,S.BIENERT,A.WATERHOUSE,K.ARNOLD,G.STUDER,
JRNL  AUTH 2 T.SCHMIDT,F.KIEFER,T.GALLO
CASSARINO,M.BERTONI,L.BORDOLI,
JRNL  AUTH 3 T.SCHWEDE
JRNL  TITL  SWISS-MODEL: MODELLING PROTEIN TERTIARY
AND QUATERNARY
JRNL  TITL 2 STRUCTURE USING EVOLUTIONARY
INFORMATION
JRNL  REF  NUCLEIC.ACIDS.RES  2014
JRNL  REFN  ISSN 0305-1048
JRNL  PMID  24782522
JRNL  DOI  10.1093/nar/gku340
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REMARK  3 MODEL INFORMATION
REMARK  3 ENGIN  PROMOD3
REMARK  3 VERSN  1.0.0
REMARK  3 OSTAT  MONOMER
REMARK  3 OSRSN  PREDICTION
REMARK  3 GMQE  0.65
REMARK  3 QMN4  -1.90
REMARK  3
REMARK  3 TEMPLATE 1
REMARK  3 PDBID  4rgd
REMARK  3 CHAIN  A
REMARK  3 MMCIF  A
REMARK  3 PDBV  2016-07-29
REMARK  3 SMTLE  4rgd.1.A
REMARK  3 SMTLV  2016-08-03
REMARK  3 MTHD  X-RAY DIFFRACTION 1.20 A
REMARK  3 FOUND  HHblits
REMARK  3 GMQE  0.65
REMARK  3 SIM  0.37
REMARK  3 SID  35.71
REMARK  3 OSTAT  homo-dimer
REMARK  3 LIGND  CIT
ATOM  1  N  THR  A  4  55.986 -2.970 89.102 1.00 0.34  N
ATOM  2  CA  THR  A  4  55.526 -2.404 87.777 1.00 0.34  C
ATOM  3  C  THR  A  4  56.617 -2.286 86.715 1.00 0.34  C
ATOM  4  O  THR  A  4  56.298 -2.050 85.596 1.00 0.34  O
ATOM  5  CB  THR  A  4  54.855 -1.023 87.967 1.00 0.34  C
ATOM  6  OG1 THR  A  4  55.684 -0.173 88.743 1.00 0.34  O
ATOM  7  CG2 THR  A  4  53.540 -1.159 88.758 1.00 0.34  C
ATOM  8  N  GLY  A  5  57.944 -2.498 87.008 1.00 0.40  N
ATOM  9  CA  GLY  A  5  58.934 -2.311 85.933 1.00 0.40  C
ATOM 10  C  GLY  A  5  59.203 -0.881 85.550 1.00 0.40  C
ATOM 11  O  GLY  A  5  59.780 -0.607 84.506 1.00 0.40  O
ATOM 12  N  MET  A  6  58.809  0.081 86.409 1.00 0.53  N
ATOM 13  CA  MET  A  6  59.205  1.459 86.267 1.00 0.53  C
ATOM 14  C  MET  A  6  60.640  1.570 86.645 1.00 0.53  C
ATOM 15  O  MET  A  6  61.020  1.242 87.759 1.00 0.53  O
ATOM 16  CB  MET  A  6  58.385  2.407 87.176 1.00 0.53  C

```

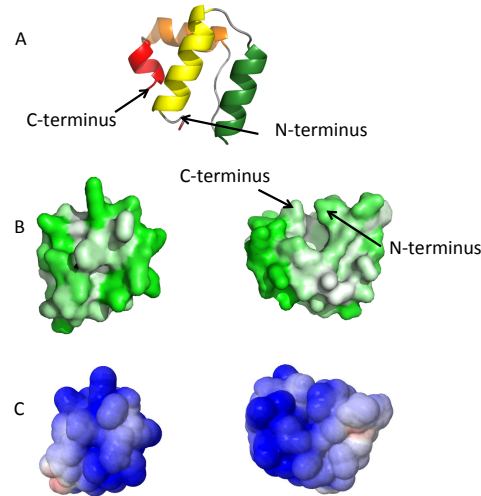








B)



**Figure S5-** Structural models of garvacin ML. A) Ribbon diagram depicting the saposin-like fold. The C- and N- termini are explicitly shown. Hydrophobic surface (B) and electrostatic potential surface (C) maps of garvacin ML. Orientation peptide backbone in surface filling diagrams, B and C, correlate to one another.

## 6.Mutacin BhtB

### A) PDB file for model of Mutacin BhtB. Structure modeled after lacticin Q using SWISS-MODEL<sup>84</sup>

```

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TITLE  2 Untitled Project
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AUTHOR  SWISS-MODEL SERVER (SEE REFERENCE IN JRNL
Records)
REVDAT  1 15-AUG-16 1MOD  1  21:39
JRNL  AUTH
M.BIASINI,S.BIENERT,A.WATERHOUSE,K.ARNOLD,G.STUDER,
JRNL  AUTH 2 T.SCHMIDT,F.KIEFER,T.GALLO
CASSARINO,M.BERTONI,L.BORDOLI,
JRNL  AUTH 3 T.SCHWEDE
JRNL  TITL  SWISS-MODEL: MODELLING PROTEIN TERTIARY
AND QUATERNARY
JRNL  TITL 2 STRUCTURE USING EVOLUTIONARY
INFORMATION
JRNL  REF  NUCLEIC.ACIDS.RES  2014
JRNL  REFN  ISSN 0305-1048
JRNL  PMID  24782522
JRNL  DOI  10.1093/nar/gku340
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REMARK  3 OSTAT  MONOMER
REMARK  3 OSRSN  USER
REMARK  3 GMQE  0.74
REMARK  3 QMN4  -1.71
REMARK  3
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REMARK  3 PDBID  2n8p
REMARK  3 CHAIN  A
REMARK  3 MMCIF  A
REMARK  3 PDBV  2016-08-12
REMARK  3 SMTLE  2n8p.1.A
REMARK  3 SMTLV  2016-08-14
REMARK  3 MTHD  SOLUTION NMR 0.00 A
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REMARK  3 GMQE  0.74
REMARK  3 SIM  0.43
REMARK  3 SID  45.24
REMARK  3 OSTAT  monomer
ATOM  1  N  TRP A  2  9.109 -0.818 -0.130 1.00 0.48  N
ATOM  2  CA  TRP A  2  10.436 -1.289 -0.665 1.00 0.48  C
ATOM  3  C  TRP A  2  10.867 -0.538 -1.927 1.00 0.48  C
ATOM  4  O  TRP A  2  11.803 0.265 -1.816 1.00 0.48  O
ATOM  5  CB  TRP A  2  10.478 -2.840 -0.737 1.00 0.48  C
ATOM  6  CG  TRP A  2  11.868 -3.431 -0.982 1.00 0.48  C
ATOM  7  CD1  TRP A  2  13.012 -3.412 -0.217 1.00 0.48  C
ATOM  8  CD2  TRP A  2  12.196 -4.175 -2.166 1.00 0.48  C
ATOM  9  NE1  TRP A  2  14.021 -4.105 -0.853 1.00 0.48  N
ATOM  10  CE2  TRP A  2  13.539 -4.578 -2.042 1.00 0.48  C
ATOM  11  CE3  TRP A  2  11.445 -4.512 -3.289 1.00 0.48  C
ATOM  12  CZ2  TRP A  2  14.154 -5.326 -3.029 1.00 0.48  C
ATOM  13  CZ3  TRP A  2  12.069 -5.276 -4.285 1.00 0.48  C
ATOM  14  CH2  TRP A  2  13.401 -5.686 -4.152 1.00 0.48  C
ATOM  15  N  GLY A  3  10.233 -0.618 -3.127 1.00 0.61  N
ATOM  16  CA  GLY A  3  10.771 0.129 -4.291 1.00 0.61  C
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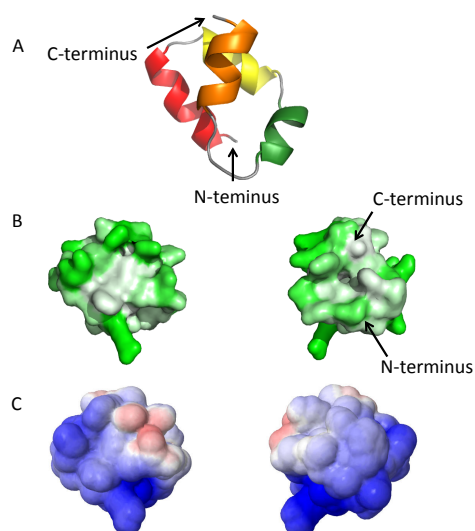
```











**Figure S6-** Structural models of mutacin BhtB. A) Ribbon diagram depicting the saposin-like fold. The C- and N- termini are explicitly shown. Hydrophobic surface (B) and electrostatic potential surface (C) maps of mutacin BhtB. Orientation peptide backbone in surface filling diagrams, B and C, correlate to one another.

References:

84 M. Biasini, S. Bienert, A. Waterhouse, K. Arnold, G. Studer, T. Schmidt, F. Kiefer, T. G. Cassarino, M. Bertoni, L. Bordoli and T. Schwede, *Nucleic Acids Res.*, 2014, **42**, 252–258.

85 H. M. Berman, J. Westbrook, Z. Feng, G. Gilliland, T. N. Bhat, H. Weissig, I. N. Shindyalov and P. E. Bourne, *Nucleic Acids Res.*, 2000, **28**, 235–242.